

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2003, 15:50:54 ; Search time 2481.53 seconds  
(without alignments)  
16465.78 Million cell updates/sec

Title: US-09-497-967-3

Perfect score: 1404

Sequence: 1 atgaaaataataatttagt.....tgattcttattattatta 1404

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sv:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_or:\*  
21: em\_ov:\*  
22: em\_pat:\*  
23: em\_ph:\*  
24: em\_pl:\*  
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26: em\_sts:\*  
27: em\_un:\*  
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29: em\_htg\_hum:\*  
30: em\_htg\_inv:\*  
31: em\_htg\_other:\*  
32: em\_htg\_mus:\*  
33: em\_htg\_pln:\*  
34: em\_htg\_rtd:\*  
35: em\_htg\_mam:\*  
36: em\_htg\_vrt:\*  
37: em\_sy:\*  
38: em\_htgo\_hum:\*  
39: em\_htgo\_mus:\*  
40: em\_htgo\_pln:\*  
41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1404	100.0	3026	3	AF324424	AF324424 Ichthyoph
2	254.4	18.1	1520	3	AF405431	AF405431 Ichthyoph
3	252.6	18.0	2486	3	AF140273	AF140273 Ichthyoph
4	214.6	15.3	1249	3	ICVIMANT	M92907 Ichthyophth
5	96	6.8	175748	2	AC120669	AC120669 Rattus no
6	96	6.8	180903	2	AC120659	AC120659 Rattus no
7	95.2	6.8	186935	2	AC022322	AC022322 Homo sapi
8	92.4	6.6	179553	2	AC024253	AC024253 Homo sapi
9	90.8	6.5	131274	2	AC096869	AC096869 Rattus no
10	90.8	6.5	176822	2	AC099174	AC099174 Rattus no
11	85.6	6.1	261604	2	AC119819	AC119819 Mus muscu
12	85.4	6.1	127354	2	AC117014	AC117014 Rattus no
13	85.4	6.1	155019	2	AC117361	AC117361 Rattus no
14	81	5.8	35793	5	AY016024	AY016024 Takifugu
15	81	5.8	84472	2	AC096684	AC096684 Takifugu
16	80.2	5.7	132449	9	AL365272	AL365272 Human DNA
17	77.2	5.5	22398	5	FR0271723	AJ271723 Fugu rubr
18	77	5.5	85786	9	AL162582	AL162582 Human DNA
19	76.6	5.5	10115	5	AF397467	AF397467 Ictalurus
20	75.8	5.4	183413	2	AC131200	AC131200 Rattus no
21	75.6	5.4	170985	2	AC096032	AC096032 Rattus no
22	74.6	5.3	204259	2	AC110817	AC110817 Mus muscu
23	74	5.3	172307	2	AC044842	AC044842 Homo sapi
24	72.4	5.2	189461	2	AC119627	AC119627 Rattus no
25	72.4	5.2	191841	2	AC121374	AC121374 Rattus no
26	72	5.1	134558	2	AC125757	AC125757 Rattus no
27	72	5.1	180668	2	AC020857	AC020857 Mus muscu
28	69.8	5.0	666	8	AF41305052	AF413051 Zea mays
29	69.2	4.9	172853	9	AC084361	AC084361 Homo sapi
30	68.2	4.9	71553	2	AC096997	AC096997 Takifugu
31	68	4.8	154141	2	AC121042	AC121042 Rattus no
32	68	4.8	162269	9	AC000097	AC000097 Homo sapi
33	67.8	4.8	184830	2	AC113220	AC113220 Rattus no
34	67.2	4.8	185994	2	AC002042	AC002042 Homo sapi
35	67.2	4.8	300994	2	AC129317	AC129317 Mus muscu
36	66.2	4.7	131346	2	AC119558	AC119558 Rattus no
37	66	4.7	158615	2	AC117835	AC117835 Rattus no
38	65.8	4.7	101534	2	AC108576	AC108576 Rattus no
39	65.8	4.7	298283	3	AF003782	AF003782 Drosophil
40	64.8	4.6	177035	2	AC099443	AC099443 Rattus no
41	64.4	4.6	186558	2	AC079031	AC079031 Homo sapi
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43	64.2	4.6	187617	2	AC118993	AC118993 Rattus no
44	64	4.6	100726	2	AC116961	AC116961 Dictyoste
45	63.8	4.5	177435	2	AC128321	AC128321 Rattus no

# ALIGNMENTS

RESULT 1  
AF324424  
LOCUS  
DEFINITION  
3026 bp DNA linear INV 27-FEB-2002  
Ichthyophthirius multifiliis immobilization antigen isoform  
(TAG52A) gene, complete cds.  
ACCESSION  
AF324424  
VERSION  
AF324424.1 GI:12698726  
KEYWORDS  
SOURCE  
ichthyophthirius multifiliis.  
ORGANISM  
Ichthyophthirius multifiliis  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Ophryoglenina; Ichthyophthirius.  
REFERENCE  
1 (bases 1 to 3026)  
AUTHORS  
Lin, Y., Lin, T.L., Wang, C.C., Wang, X., Stieger, K., Klopfeisch, R.  
and Clark, T.G.

TITLE Variation in primary sequence and tandem repeat copy number among  
i-antigens of Ichthyophthirius multifiliis  
JOURNAL Mol. Biochem. Parasitol. 120 (1), 93-106 (2002)  
MEDLINE 21839613  
PUBMED 11849709  
REFERENCE 2 (bases 1 to 3026)  
AUTHORS Lin, Y., Lin, T.-L. and Clark, T. G.  
TITLE Direct Submission  
SUBMITTED (27-NOV-2000) Microbiology and Immunology, NYSCVM Cornell  
UNIVERSITY, Ithaca, NY 14853, USA  
FEATURES  
Location/Qualifiers  
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/macronuclear  
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/isolate="G5"  
/db\_xref="taxon:5932"  
1285..2817  
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1330..2736  
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/codon\_start=1  
/transl\_table=6  
/product="immobilization antigen isoform"  
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CAANFYDGNNTFQAGSRCKCPANKVQAVATAGGTATLIAQCALEPAGVFLTDGT  
TSYKQAASECVKCAANFYTTKQTDWVAGIDTCTSCNKLITSGAEANILPESAKKNIQ  
DFANFLISILLISYLL"  
BASE COUNT 1177 a 316 c 355 g 1178 t  
ORIGIN  
Query Match 100.0%; Score 1404; DB 3; Length 3026;  
Best Local Similarity 100.0%; Pred. No. 1.le-237;  
Matches 1404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGAAATAATATTTAGTAATATTCATTATTTTCATTATTTATCAATTAATAATCT 60  
Db 1330 ATGAAATAATATTTAGTAATATTCATTATTTTCATTATTTATCAATTAATAATCT 1389  
Qy 61 GCTAATGTCCTGTGGAATGAACTAACACAGCCGGATAAGTTGATGATCTAGGAAC 120  
Db 1390 GCTAATGTCCTGTGGAATGAACTAACACAGCCGGATAAGTTGATGATCTAGGAAC 1449  
Qy 121 CCTGCAATGCTGTAATGTTAGAAAACCTTTTATTAATTAATGCTGCTTTCGTT 180  
Db 1450 CCTGCAATGCTGTAATGTTAGAAAACCTTTTATTAATTAATGCTGCTTTCGTT 1509  
Qy 181 CCTGGTGTAGTACGTGTACACCTTGCCATAAAAAAGATGCTGCTTAAACCAAT 240  
Db 1510 CCTGGTGTAGTACGTGTACACCTTGCCATAAAAAAGATGCTGCTTAAACCAAT 1569  
Qy 241 CCACCTGTACTGCTAATTTAGTCACATAATGTAACGTTAAATGCCCTGCTGGTACCGCA 300  
Db 1570 CCACCTGTACTGCTAATTTAGTCACATAATGTAACGTTAAATGCCCTGCTGGTACCGCA 1629  
Qy 301 ATTGCAGTGGAGCAACAGATTTATGACGAATAATACAGAACTGTATTTAGTAAT 360  
Db 1630 ATTGCAGTGGAGCAACAGATTTATGACGAATAATACAGAACTGTATTTAGTAAT 1689  
Qy 361 AATTTTATAATGAAATGCTCCAAATTTTAAATGACGTGCTAGTACATGCACAGCTGT 420  
Db 1690 AATTTTATAATGAAATGCTCCAAATTTTAAATGACGTGCTAGTACATGCACAGCTGT 1749

Qy 421 CCGGTAAACAGAGTTGGTGGTGCATTTGACTGCTGGTAAATGCCGCTACCATAGTCGCATAA 480  
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Qy 481 TGTAACTGCGCATGTCCTTACTGGTACTGCACTTGCATGATGAGTAACACTACTGATTATGTT 540  
Db 1810 TGTAACTGCGCATGTCCTTACTGGTACTGCACTTGCATGATGAGTAACACTACTGATTATGTT 1869  
Qy 541 AGATCAATTCACAGATGTTAAATGTAAGTAACTTAACTTTTACTATAATGTTGTAATAATGGT 600  
Db 1870 AGATCAATTCACAGATGTTAAATGTAAGTAACTTAACTTTTACTATAATGTTGTAATAATGGT 1929  
Qy 601 AATACTCCTTTCAATCCAGGTTAAAGTTAAATGACACACCTTGTCCGGCAATTTAAACCTGCT 660  
Db 1930 AATACTCCTTTCAATCCAGGTTAAAGTTAAATGACACACCTTGTCCGGCAATTTAAACCTGCT 1989  
Qy 661 AATGTTGCTTAAAGTAACTTTAGGTAATGATGCTACATAACCGCATATGTAACGTTGCA 720  
Db 1990 AATGTTGCTTAAAGTAACTTTAGGTAATGATGCTACATAACCGCATATGTAACGTTGCA 2049  
Qy 721 TGCCCTGATGTTACTATAAGTCTGCTGGAGTAAATAATTTGGTAGCACAAAACACTGAA 780  
Db 2050 TGCCCTGATGTTACTATAAGTCTGCTGGAGTAAATAATTTGGTAGCACAAAACACTGAA 2109  
Qy 781 TGTACTAATTTGCTCCTAACTTTTACAAATAATTAATGCTCCTTAATTTCAATCCAGGTAAT 840  
Db 2110 TGTACTAATTTGCTCCTAACTTTTACAAATAATTAATGCTCCTTAATTTCAATCCAGGTAAT 2169  
Qy 841 AGTACATGCTTACCTTCCCGCAAAATAAGATTAATGCTGCTGAAGCCACTGCAAGTGGT 900  
Db 2170 AGTACATGCTTACCTTCCCGCAAAATAAGATTAATGCTGCTGAAGCCACTGCAAGTGGT 2229  
Qy 901 GCGGTACTTTAGCCAAATAATGTAATTTGTCATGCCCTGATGCTGCTGCTGCTGCTGCTGCT 960  
Db 2230 GCGGTACTTTAGCCAAATAATGTAATTTGTCATGCCCTGATGCTGCTGCTGCTGCTGCTGCT 2289  
Qy 961 GGAGCAACTAATTTATGTAATTTAATACAGATGCTTAAATTTGCTGCTGCTGCTGCTGCTGCT 1020  
Db 2290 GGAGCAACTAATTTATGTAATTTAATACAGATGCTTAAATTTGCTGCTGCTGCTGCTGCTGCT 2349  
Qy 1021 TTTGATGTTAATAATTTCTAGCGAGAGTAGTAGATGCAAGCATGCTCCAGCAATAATAA 1080  
Db 2350 TTTGATGTTAATAATTTCTAGCGAGAGTAGTAGATGCAAGCATGCTCCAGCAATAATAA 2409  
Qy 1081 GTTTAAGCGCTGTAGCAACTGCAGTGGTACTGCTACTTTAAATTTGCAATGTCGCCCTT 1140  
Db 2410 GTTTAAGCGCTGTAGCAACTGCAGTGGTACTGCTACTTTAAATTTGCAATGTCGCCCTT 2469  
Qy 1141 GAATGCCCTGCTGGTACTGCTACTCAGGATGGAACAACATCTACTTATAATAAAGCAGCA 1200  
Db 2470 GAATGCCCTGCTGGTACTGCTACTCAGGATGGAACAACATCTACTTATAATAAAGCAGCA 2529  
Qy 1201 TCTGAATGTTAAATGCTGCCAACTTTTATCTACAAAAATAAAGTGGGTAGCA 1260  
Db 2530 TCTGAATGTTAAATGCTGCCAACTTTTATCTACAAAAATAAAGTGGGTAGCA 2589  
Qy 1261 GGTATTGATACATGTAAGTGTGTAATAAAAAATTAACCTTCGGCGCTCAAGCTAATTTA 1320  
Db 2590 GGTATTGATACATGTAAGTGTGTAATAAAAAATTAACCTTCGGCGCTCAAGCTAATTTA 2649  
Qy 1321 CCTGAATGCTAAAAAATAATATGATGCTGCTAAATTTTATCAATTTCCCTTA 1380  
Db 2650 CCTGAATGCTAAAAAATAATATGATGCTGCTAAATTTTATCAATTTCCCTTA 2709  
Qy 1381 TTATTGATTTCTTATTATTATTA 1404  
Db 2710 TTATTGATTTCTTATTATTATTA 2733

DEFINITION Ichthyophthirius multifiliis 52kDa immobilization antigen variant B  
ACCESSION AF405431  
VERSION AF405431.1 GI:15290741  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
Source  
CDS  
BASE COUNT 493 a 255 c 256 g 516 t  
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Query Match 18.18; Score 254.4; DB 3; Length 1520;  
Best Local Similarity 55.18; Pred. No. 3e-35;  
Matches 794; Conservative 0; Mismatches 546; Indels 102; Gaps 11;  
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DB 41 ATGAAATTAATATTTTAAATAATTTTCATTATTTTCCTTATTTATTAAGTAATGAAGCT 100  
QY 61 GCTAATTCCTGTTGGAAGTAACTAACACAGCCGGATAAGTTGATGATCTAGGAAT 120  
DB 101 GTTAATGCTTAATGGTGTGCAATTCGGAATGGATAAATCTGATACAGGAGCTGCAGAT 160  
QY 121 CCTGCAAAATGTTGTTAGTAACTTTTACAAAACCTTTTATTAATAATAATGCTGCTGCT----- 174  
DB 161 ATAATACTGTACTCATGCTAAACACACTTTTACTTTTAAATGGTGTAACTCTGCAGGT 220  
QY 175 -----TTGTTTCCTGGTGTAGTACGTGCTACACCTGTGTCATAA 213  
DB 221 CAGGCTCCTGCTGTGTACAAATTCAGAGGTTAGTCAGTGCATAGCTTGCCAAAGTA 280  
QY 214 AAAAAGATGCTGCTGTTTAAACAAATCCACCTGCTACTGCTTAATTTAGTCACATAATGT 273  
DB 281 CACAAA---GCCGATTCACACAGATAAGGTGGTGTGCTGAATTTAGCCCGCATAATGT 337  
QY 274 AACGTTAAATGCCCTGCTGCTACCGCAATTTGCAGGTGGAGCAACAGATTATCCAGCAATA 333

DB 338 AGCAACTATATGTCCTGCTGCACCTGCAGTTGAAGATGGATCACCCTACTTTTACTTAATCC 397  
QY 334 ATCACAGATGTTGTTAATTTTATAGATTAATTTTATTAATAAGTAAATGCTCCAAATTTTAA 393  
DB 398 CTCACATAATGTTGTTAATTTGTAACCTAACTTTTACTTTAATGGTGGTAATCCTACAGGT 457  
QY 394 GCAGGTGCTAGTACATGCACAGCTTCTCGGTAACACAGAGTTGGTGGTCCATTTGACTGCT 453  
DB 458 CAGGCTCCTGGTCTGGATAATTCGATCCCACTTAATGATTGCAAAATCCTGATCTTCT 517  
QY 454 GGTAAATGCCGCTACCATAGTCGCATAAATGAACGTCGCATGCTCTACTGCTACTGCATCT 513  
DB 518 AATAATCC-----TGAAGTTCCCTAATGTTTCTAGCCCTAATGGTTAATGCCGA 565  
QY 514 GATGATGGAGTAACACTACTGATTATGTTAGATCATTTACAGAGATGTTTAAATGTAGACTT 573  
DB 566 GCTTGTGCTAAGTAACA---AGTCTGATTCTCAATTAAGACCCAGGTGCTTAGGCTAAATTTA 622  
QY 574 AACTTTTACTAATAAGTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 633  
DB 623 GCCACATAATGTAACAATGAATGCTCTACTGGCACTGCTATTCAGACGGAGCAATATTT 682  
QY 534 ACACCTTGTCCGGCAATTAACCTGCTAATGTTGCTTAAAGCTACTTTTAAAGTAAATGATCT 693  
DB 683 ATTTATGCTAATCAATCTCATAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 742  
QY 694 ACAATAACCGCATAAATGTAACGTTGCATGCCCTGATGCTACTATAGTGTGCTGCTGGAGTA 753  
DB 743 -----GGCAATCCTTCAGCTCAGAAATCCTGGTAATGGA 775  
QY 754 AATAATGGGTAGCACAAAACACTGAATGTACTAATTTGCTGCTCCTACTTTTACAATAAT 813  
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DB 836 ATGGTTCC-----TGGCCCTAATAGTAATAGTAAATGCGGTAGCTTCCGAATCAAAAAGACC 886  
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DB 887 AA---TTCTTAATCCAGATCAGGCTCTGAGGCTAATTTAGCCGCTAATGTTGGCACTGAA 943  
QY 934 TCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 990  
DB 944 TGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1003  
QY 991 GAATGCT 1050  
DB 1004 TAATGCTGTTAATTTGTAAGCTGGCTTTTACT---AAATAGTAAATTTTCGAAGCAGGTAA 1060  
QY 1051 AGTAGATGCAAAAGATGTCAGCAAAATAAGTTTAAAGCGCTGTAGCAACTGCAGGCTGGT 1110  
DB 1061 AGTTAATGCAATAAGTGTGCAAGTAAATAAACT---GGTTTCAGCACTGCTGCTCCAGGTAA 1117  
QY 1111 ACTGCTACTTTAATTTGCTAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1170  
DB 1118 AGTCTACTTTCAGCCACATATGTTTAAACAGATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1177  
QY 1171 GGAACAACATCTACTTTAATAAAGCAGCATCTGAATGCTGTTAAATGCTGCTGCTGCTGCTGCTGCT 1230  
DB 1178 GGTACATCACTAATTTTGTAGCTTTTAGCAAGTGAATGCTAATGTTAGGCTAACITTT 1237  
QY 1231 TATACTACAAAATAAATGATGTTGGGTAGCAGGTATTTGATACATGCTACTAGTTGTATAATAA 1290  
DB 1238 TATGATCAAAAACATCTGCTTTTGCAGCAGGTACTGATACATGCTACTGAATGTTCTTAA 1297  
QY 1291 AAATTAATCTTCTGCGCTGAAGCTAATTTACCTGAATCTGCTTAAAAAATAATATAATGT 1350  
DB 1298 AAATTAATCTTCTGCTGCTACAGCTAAAGTATATGCTGAAGCTACTTAAAGCAATAATGC 1357  
QY 1351 G-----ATTTCGCTAATTTTTTATCAATTTTCTTATTTATTTATTTATTTATTTATTTA 1401

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us-09-497-967-3.rge

Db 1358 GCCAGTTCACCTTCGCAAAATTTTATCAATGTCCTTAATATTATTTCTTCTATTG 1417

QY 1402 TT 1403

Db 1418 TT 1419

RESULT 3

AF140273

LOCUS

DEFINITION

Ichthyophthirius multifiliis immobilization antigen precursor (IAG48) gene, complete cds.

ACCESSION

AF140273.1

VERSION

AF140273.1

KEYWORDS

ORGANISM

Ichthyophthirius multifiliis.

SOURCE

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Ophryoglenina; Ichthyophthirius.

REFERENCE

AUTHORS

Clark, T.G., Lin, T.L., Jackwood, D.A., Sherrill, J., Lin, Y. and Dickerson, H.W.

TITLE

The gene for an abundant parasite coat protein predicts tandemly repetitive metal binding domains

JOURNAL

MEDLINE

99196987

PUBMED

10095108

REFERENCE

2 (bases 1 to 2486)

AUTHORS

Gaertig, J., Gao, Y., Tishgarten, T., Clark, T.G. and Dickerson, H.W.

TITLE

Surface display of a parasite antigen in the ciliate Tetrahymena thermophila

JOURNAL

REFERENCE

3 (bases 1 to 2486)

AUTHORS

Clark, T.G., Lin, T.-L., Jackwood, D.A. and Dickerson, H.W.

TITLE

Direct Submission

JOURNAL

Submitted (29-MAR-1999) Microbiology & Immunology, Cornell University, College of Veterinary Medicine, Ithaca, NY 14853, USA

FEATURES

source

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/isolate="G1"

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/product="immobilization antigen precursor"

433..1761

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/note="surface protein; 48 kDa i-antigen"

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/transl\_table=6

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/db\_xref="GI:4868371"

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493..1758

/gene="IAG48"

/product="immobilization antigen"

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BASE COUNT

ORIGIN

Query Match 18.08; Score 252.6; DB 3; Length 2486;

Best Local Similarity 56.7%; Pred. No. 5.6e-35; Matches 660; Conservative 0; Mismatches 394; Indels 111; Gaps 6;

QY 344 GTGTTAATTTGTAATTAATTTTATATAATGAAATGCTCCAAATTTTAAATGCGAGGTGCTA 403

Db 599 GFGCTGCTTAAGGAGAACCTAATGGTAATTAACCTTTTCGAGCAAAATATGCTGTAGAG 658

QY 404 GTACATGCACAGCTGTGTCGGTAAACAGAGATTGGTGTGCAATGACACTGCTGGTAATGCCG 463

Db 659 GTATATGTTGTAACCATGCGCAAAATAAACAGAGTAGGCTCTGTACCAATGCAAGGTGACTTAG 718

QY 464 CTACCATAGTCGCATAATGTAACGTCGCAATGCTACTGTTGCTACTGCTACTGATGATGAG 523

Db 719 CTACTTTAGCCACATAATGTCAGTACTTAATGTCCTACTGTCGCACTGCACTTGTATGATGAG 778

QY 524 TAACTACTGATTATGTTAGATCATTCACAGAAATGTTAAATGATGACACTTAACCTTTTACT 583

Db 779 TGACAGATGTTTTGATAGATCAGCGCATATGTTGTAATGCAAACTTAACCTTTTACT 838

QY 584 ATAATGGTAATTAATGGTAATGCTCTCTTCAATCCAGGTAAAGTTAATGCACACCTTGTG 643

Db 839 ATAATGGTGTCTCTCTTAAAGGTGAAGCTCTCGCGTTTAAAGTTTGTGCTGCTGCTG 898

QY 644 CGCAATTAACCTGCT-----AATG 664

Db 899 CGCTGCGAGGTGTTGCTGCCGTTTACTAGTTAATGTTGACCTTGCCAACTAAACAAAACG 958

QY 665 TTGCTTAACTACTTTTAGTAAATGATGCTACAAATAACCGCATATGTAACCTTGCATGCC 724

Db 959 ATTCTCTCCCACTGCAGGTGCTTAAGCTAATTTAGCCACATAATGTAGCAATTAATGTC 1018

QY 725 CTGATGGTACTATAAGTGTGCTGCGAGT---AAATAATGGGTAGCACAAAACACTGAAT 781

Db 1019 CTACTGCCACTGTACTGTATGATGATGGAGTGCACCTTGTGTTTAAATACATCAGCCACATAT 1078

QY 782 GTACTAATGTCCTCTAACTTTTACAATAATAATGCTCTCTAAAT-----826

Db 1079 GTGTTAAATGCACACCTAATCTTTACTATAATGGTGGTCTCTCTTAAGGTGAAGCTCCTG 1138

QY 827 -----TCATCCAGGTATAGTACAT 847

Db 1139 GCGTTTAAAGTTTGTGCTGCTGCCGCTGCGAGGTGTTGCTGCCGTTACTAGTTAAT 1198

QY 848 GCTACTCTGCCAGCAAAATAAAGATTATGTTGCTGAAGCCACTGCAGTGTGCGCGCTA 907

Db 1199 GTGTACCTTGCCAAATAAACAAAACGATTCCT---GCCACTGCAGTGCCTAAGCTA 1255

QY 908 CTTTAGCAAAATAATGTAATTTGCAATGCCCTGATGGTACTGCAATGCTAGTGGACAA 967

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QY 968 CTAATTATGTAATTTATAACAGAAATGCTAAATGTCGCTAACTTTTATTTTATG 1027

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QY 1028 GTAATAATTTCTAGGCAAGTAGTAGTGAAGCATGTCAGCAAAATAAAGTTTAAAG 1087

Db 1376 ATGTTAATTTGCAAGCAGGTAAAGTTAATGTTTAAAGTGTCCAGTGAAGTAAACT---A 1432

QY 1088 GCGCTGTAGCAACTGCAGGTGGTACTGCTACTTAAATGCAATAATGTCCTTGTATGCC 1147

Db 1433 CTCAGCACATGCTCCAGGTAAATGCTACTTAAAGCCACATAATGTTTGAACCATATGC 1492

QY 1148 CTGCTGTACTGTACTCACCGATGGAACACATCTACTTATAAATAAGCAGCATCTGAAT 1207

Db 1493 CTGCTGGTACAGTACTTGATGATGGAACATCACTAATTTTGTAGCTTCGCAACTGAAT 1552

QY 1208 GTGTTAAATGTCGCCAACTTTTATATCTACAAATAAATGATTTGGGTAGCAGGTATTG 1267

Db 1553 GTACTAATGTTCTGCTGGCTTTTTCATCAAAACAACTGGTTTACAGCAGGTACTG 1612

QY 1268 ATACATGCTACTAGTTGTAATAAAAAAATACTTCTGCGCTGAAGCTTAATTTACCTGAAT 1327



Db	946	CTCCAGCACATGCTCCAGGTAATACTGCTACTTAAGCCACATAATGTTTGACCACATGTC	1005
QY	1148	CTGCTGGTACTGTACTCACCAGTGAACAACATCTACTTATAATAAGCAGCATCTGAAT	1207
Db	1006	CTGCTGGTACAGTACTTGATGATGGAACATCAACTAATTTTGTAGCTTCGCGCAACTGAAT	1065
QY	1208	GTGTTAAATGTGCTGCCAACTTTTATATCTACTACAAATAAATGATTTGGGTAGCAGGTAATG	1267
Db	1066	GTACTAAATGTTCTGCTGGCTTTTTCATCAAAAAACAACCTGTTTACAGCAGGTAAGT	1125
QY	1268	ATACATGTACTAGTTGTAATAAAAAAATTAACCTTCGCGCCTGAAGCT	1314
Db	1126	ATACATGTACTAGTACTAAAAAATTAACCTTCGTGCGCACAGCT	1172
RESULT 5			
LOCUS	AC120669/c	175748 bp	DNA linear HTG 23-JUL-2002
DEFINITION	Rattus norvegicus clone CH230-22G10, *** SEQUENCING IN PROGRESS		
***, 46 unordered pieces.			
ACCESSION	AC120669		
VERSION	AC120669.2 GI:21902861		
KEYWORDS	HTG; HTGS_PHASE1.		
SOURCE	Rattus norvegicus.		
ORGANISM	Rattus norvegicus		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
Rattus.			
REFERENCE	1 (bases 1 to 175748)		
AUTHORS	Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,		
Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayele,M., Banks,T.,			
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Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,			
Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q.,			
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,			
Williams,G., Williamson,A., Wlarczyk,R., Wooden,S., Worley,K.,			
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,			
Weinstock,G. and Gibbs,R.			
Direct Submission			
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 175748)		
AUTHORS	Worley,K.C.		
TITLE			
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 180903)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amarantunge,H.C., Are,J.K., Ayale,K., Banks,T., Barbaria,J., Benton,J., Blmage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brleva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carton,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,K., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,B., Dexter,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Girelli,J.H., Guevara,W., Gundaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Martindale,A., Martinez,E., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Meigs,G., Metzker,M., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Morgan,M., Morris,S., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoostari,N., Sisson,I., Sodergren,E., Sonalike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalón,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Woodson,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.

Direct Submission

Unpublished

2 (bases 1 to 180903)

Worley,K.C.

Direct Submission

Submitted (02-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 180903)

Worley,K.C.

Direct Submission

Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information

Center project name: GWUQ

Center clone name: CH230-35H21

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 117810 bases at least Q40

Consensus quality: 124839 bases at least Q30

Consensus quality: 130161 bases at least Q20

-----

NOTE: Estimated insert size may differ from sequence length (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).

NOTE: This is a 'working draft' sequence. It currently consists of 69 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1

1019: contig of 1018 bp in length

1118: gap of unknown length

2397: contig of 1279 bp in length

2497: gap of unknown length

3536: contig of 1039 bp in length

3536: gap of unknown length

3537: contig of 1402 bp in length

5038: gap of unknown length

5138: contig of 1278 bp in length

6416: contig of 1266 bp in length

6517: contig of 1266 bp in length

7782: gap of unknown length

7883: contig of 1174 bp in length

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9057: gap of unknown length

10223: contig of 1067 bp in length

10224: gap of unknown length

11849: contig of 1526 bp in length

11849: gap of unknown length

13459: contig of 1510 bp in length

13459: gap of unknown length

15061: contig of 1502 bp in length

15062: gap of unknown length

15161: contig of 1240 bp in length

16402: contig of 1001 bp in length

16502: contig of 1001 bp in length

17502: gap of unknown length

17503: contig of 1229 bp in length

17603: gap of unknown length

1831: contig of 1202 bp in length

1832: gap of unknown length

20133: contig of 1412 bp in length

21645: gap of unknown length

21646: contig of 1863 bp in length

21746: gap of unknown length

23708: contig of 1513 bp in length

25221: contig of 1443 bp in length

25321: gap of unknown length

26764: gap of unknown length

26864: contig of 1385 bp in length

28249: gap of unknown length

28350: contig of 1665 bp in length

30014: gap of unknown length

30114: contig of 1916 bp in length

32030: gap of unknown length

32031: contig of 3113 bp in length

35243: gap of unknown length

35343: contig of 2182 bp in length

35344: gap of unknown length

37525: contig of 1780 bp in length

37526: gap of unknown length

39406: contig of 1748 bp in length

39506: gap of unknown length

41253: contig of 1838 bp in length

41354: contig of 1627 bp in length

43192: contig of 1627 bp in length

43292: gap of unknown length

44919: contig of 1772 bp in length

45019: gap of unknown length

46791: contig of 1876 bp in length

46890: gap of unknown length

48767: contig of 1438 bp in length

50304: contig of 1438 bp in length

50404: gap of unknown length



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* 105311 105312: gap of unknown length

Query Match      6.8%; Score 96; DB 2: Length 180903;
Best Local Similarity 40.1%; Pred. No. 8.5e-08;
Matches 398; Conservative 0; Mismatches 590; Indels 4; Gaps 1;

QY 369 TAATGAAATGTCCTCAATTTTAAATGTCAGGTGCTAGTACATGCACAGCTTGTCCGGTAAA 428
Db 149053 TATTAATGCTGCTACTATTTGCTACTGCTGCTACTACTACTACTACTACTACTACTG 148994

QY 429 CAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148993
Db 148993 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148994

QY 489 CGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148993
Db 148933 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148974

QY 549 CAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148934
Db 148873 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 148814

QY 609 TTCAATCCAGCTAAAGCTTAATGCACACCTTGTCCGCGCAATTAACCTGCTGCTGCTGCT 668
Db 148813 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 148754

QY 669 TTAAGCTACTTGTAGTATGCTACAAATAACCGCATAATGTAACGTTGCATGCCCTGTA 728

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Db 148753 TACAACTACTACTACTACTACTATTTATTACTACTACTGCTGCTGCTACTACT 148694
QY 729 TGGTACTATAAGTGTGCTGCTGAGTAAATTTGGTGGTAGCACAAACACTGAATGACTAA 788
Db 148693 TTATACTACTACTACTGCTGCTGCTACTACTACTGCTATTTGGCTACTACTACTGCTAC 148634
QY 789 TTGTGCTCCTAACTTTTACAAATAAATGCTCTCTAAATTTCAATCCAGGTAAATAGTACATG 848
Db 148633 TACCCTACTACTACTGCTGCTGCTACTACTACTACTGCTGCTGCTACTACTACTAT 148574
QY 849 CCTACTTGGCCCAACAAATAAGATTTATGTTGCTGGAAGCAGTGCAGGTGGTCCCGCTAC 908
Db 148573 TACTACTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148514
QY 909 TTTAGCCCAATAATG----TAATATTGCATGCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 964
Db 148513 TAACCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148454
QY 965 CAACCTAATTTATGTAATTTATAACAGAAATGCTCTAAATTTGCTGCTGCTGCTGCTGCTGCTG 1024
Db 148453 CCACCTACTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148394
QY 1025 ATGCTAATAATTTCTAGCGAGGAAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 1084
Db 148393 CTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 148334
QY 1085 AAGCGCTGTAGCAACTGCGAGGTGGTACTGCTACTTTTAATTTGCTGCTGCTGCTGCTGCTGCTG 1144
Db 148333 CTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 148274
QY 1145 GCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1204
Db 148273 CTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148214
QY 1205 AATGTGTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264
Db 148213 CTATTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 148154
QY 1265 TTGATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1324
Db 148153 CTACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 148094
QY 1325 AATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1356
Db 148093 CTACTATTACTACTACTATAGAACCTTAGGTTTC 148062

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## RESULT 7

AC022322/c

LOCUS

AC022322 Homo sapiens chromosome 6 clone RP11-317M22, WORKING DRAFT  
SEQUENCE, 16 unordered pieces.

DEFINITION

AC022322

VERSION

AC022322.3 GI:7321964

KEYWORDS

HTG; HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE

Homo sapiens.

ORGANISM

Homo sapiens.

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

COMMENT

On Mar 24, 2000 this sequence version replaced gi:7109575.

Center: Washington University Genome Sequencing Center

----- Genome Center -----

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[illegible]

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QY 759 TTGGTAGCACAACACTGAATGCTACTAATGTCCTCACTTTTACAATAATATGC 818
Db 7830 TGCTGCTGC-----TGCTGCTGCTACTGTTATTACTGCGAATTTCTGTCCTACTGCTGC 7777
QY 819 TCCTAATTTCAATCCAGGTAATAGTACATGCTACCTTGTCCCGACAATAAAGATTATGG 878
Db 7776 TGTTGCTGTTGCTGCTGCTATGTTGCTGTTGTTAAATGTGATACTATGCTGTTGCTGA 7717
QY 879 TGCTGAAGCCACTGCAGGTGTCGCGCTACTTTAGCCAAATAATGTAATATGCATGCC 938
Db 7716 TGCTGCTGTTGCTATGCTGTTGCTGCTACTGTTGCTATTTGTTGCTTTTCTTTGTTGTC 7657
QY 939 TGATGGTACTGCAATGCTAGTGAGCAACTAATATGTAATATATAACAGATGCTCT 998
Db 7656 TCTTGTGCTGCTGCTACTGATG---CTGTGGCTGCTATTAATGTTGCTGCTGCTGT 7600
QY 999 AATTTGCTGCTAACATTTATTTTGAATGTAATAATTTCTAGCGAGAAAGTAGATG 1058
Db 7599 TGCTGTTGTTACTGCTGCTATTTGTTGCTGTTATTTGCTGATGCTGCTACTGTTGCTAT 7540
QY 1059 CAAGCATGTCAGCAATAAAGTTTAAGCGCTGTAGCAACTGCAGGTGGTACTGCTAC 1118
Db 7539 TGCTGTTGCTGCTACTATTAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7480
QY 1119 TTTAATTTGCATAATGTCCTTGAATGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1178
Db 7479 TACTGTTGTTGCTACTATGCTAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAT 7420
QY 1179 ATCTACTATTAATAGCAGCATCTGATGTTGTTAAATGTGCTGCGCAACTTTTATACTAC 1238
Db 7419 TACTACTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTAC 7360
QY 1239 AAATAAATGATTTGGGTAGCAGTATTGATACATGCTACTAGTTGTAATAAATAAATAAC 1298
Db 7359 TGCTGATTTTGGCTATTTCTGCTGCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7300
QY 1299 TTCTGGCGCTGAAGCTAATTTACCTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1336
Db 7299 TGTGATCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7262

RESULT 8
AC024253 Homo sapiens chromosome 6 clone RP11-758C19, WORKING DRAFT
LOCUS AC024253
DEFINITION AC024253
ACCESSION AC024253
VERSION AC024253.4 GI:9959959
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 179553)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 179553)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Sep 1, 2000 this sequence version replaced gi:8568958.
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0758C19
----- Summary Statistics -----
Sequencing vector: M13; 100%

```

```

Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 175235 bases at least Q40
Consensus quality: 176522 bases at least Q30
Consensus quality: 177171 bases at least Q20
Insert size: 198000; agarose-fp
Quality coverage: 4.48 in Q20 bases; agarose-fp
Quality coverage: 4.99 in Q20 bases; sum-of-ctigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 7554: contig of 7554 bp in length
* 7555 7654: gap of unknown length
* 7655 16349: contig of 8695 bp in length
* 16350 16449: gap of unknown length
* 16450 26476: contig of 10026 bp in length
* 26476 35880: contig of 9305 bp in length
* 35881 62010: contig of 26030 bp in length
* 62011 90565: contig of 28455 bp in length
* 90566 117183: contig of 26518 bp in length
* 117184 163019: contig of 45736 bp in length
* 163020 163119: gap of unknown length
* 163120 166938: contig of 3819 bp in length
* 166939 167039: gap of unknown length
* 167039 169413: contig of 2274 bp in length
* 169413 171639: contig of 2227 bp in length
* 171640 179553: contig of 7814 bp in length.
* 171740 179553: contig of 7814 bp in length.

```

```

FEATURES
    source
        1..179553
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="6"
            /clone="RP11-758C19"
    misc_feature
        1..7554
            /note="assembly_name:Contig10"
    misc_feature
        7655..16349
            /note="assembly_name:Contig11"
    misc_feature
        16450..26476
            /note="assembly_name:Contig12"
    misc_feature
        26576..35880
            /note="assembly_name:Contig13"
    misc_feature
        35981..62010
            /note="assembly_name:Contig14"
    misc_feature
        62111..90565
            /note="assembly_name:Contig15"
    misc_feature
        90666..117183
            /note="assembly_name:Contig16"
    misc_feature
        117284..163019
            /note="assembly_name:Contig17"
    misc_feature
        163120..166938
            /note="assembly_name:Contig8"
            clone_end:T7
            vector_side:right
    misc_feature
        167039..169312
            /note="assembly_name:Contig6"
    misc_feature
        169413..171639
            /note="assembly_name:Contig7"

```

[illegible]



	16967	18700:	contig of 1734	bp in length
*				
Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Wallington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.				
Direct Submission				
Unpublished				
2 (bases 1 to 176822)				
Worley, K.C.				
Direct Submission				
Submitted (09-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA				
3 (bases 1 to 176822)				
Worley, K.C.				
Direct Submission				
Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA				
On Jul 11, 2002 this sequence version replaced gi:18846108.				
----- Genome Center				
Center: Baylor College of Medicine				
Center code: BCM				
Web site: <a href="http://www.hgsc.bcm.tmc.edu/">http://www.hgsc.bcm.tmc.edu/</a>				
Contact: <a href="mailto:hgsc-help@bcm.tmc.edu">hgsc-help@bcm.tmc.edu</a>				
----- Project Information				
Center project name: GZV				
Center Clone name: CH230-9811				
----- Summary Statistics				
Sequencing vector: Plasmid;				
Chemistry: Dye-terminator Big Dye; 100% of reads				
Assembly program: Phrap; version 0.990329				
Consensus quality: 115453 bases at least Q40				
Consensus quality: 125501 bases at least Q30				
Consensus quality: 133023 bases at least Q20				
-----				
* NOTE: Estimated insert size may differ from sequence length				
(see <a href="http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html">http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html</a> ).				
* consists of 77 contigs. The true order of the pieces				
* is not known and their order in this sequence record is				
* arbitrary. Gaps between the contigs are represented as				
* runs of N, but the exact sizes of the gaps are unknown.				
* This record will be updated with the finished sequence				
* as soon as it is available and the accession number will				
* be preserved.				
* 1				
* 1052: contig of 1052 bp in length				
* 1053				
* 1153				
* 2180				
* 2280				
* 3356				
* 3456				
* 4835				
* 4935				
* 6223				
* 6323				
* 7401				
* 7501				
* 8808				
* 10267				
* 10367				
* 11663				
* 11763				
* 12813				
* 12913				
* 14137				
* 14236				
* 15446				
* 15547				
* 16866				
* 16967				
* 18700: contig of 1734 bp in length				
* 18800: gap of unknown length				
* 18801				
* 20358: contig of 1558 bp in length				
* 20458: gap of unknown length				
* 20459				
* 22025: contig of 1567 bp in length				
* 22135: gap of unknown length				
* 22026				
* 22126				
* 24515: contig of 2390 bp in length				
* 24516				
* 24616				
* 25847				
* 25947				
* 27176: contig of 1230 bp in length				
* 27277				
* 28284				
* 28384				
* 29996				
* 30096				
* 31460				
* 31560				
* 32924: contig of 1365 bp in length				
* 32925				
* 33024: gap of unknown length				
* 33025				
* 34073: contig of 1049 bp in length				
* 34074				
* 34173: gap of unknown length				
* 34174				
* 35425: contig of 1252 bp in length				
* 35525: gap of unknown length				
* 35526				
* 36980: contig of 1455 bp in length				
* 36981				
* 37081				
* 38628: contig of 1548 bp in length				
* 38728: gap of unknown length				
* 38629				
* 38729				
* 40213				
* 40312: gap of unknown length				
* 40313				

[illegible]

RESULT 11  
AC119819/0  
LOCUS



```

Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: LI17592
Center clone name: 107_G_22
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 243729 bases at least Q40
Consensus quality: 251231 bases at least Q30
Consensus quality: 253857 bases at least Q20
Insert size: 220000; agarose-fp
Insert size: 255004; sum-of-contigs
Quality coverage: 8.2 in Q20 bases; agarose-fp
Quality coverage: 7.1 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 67 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 641: contig of 641 bp in length
*
* 642 741: gap of 100 bp
* 742 1156: contig of 415 bp in length
* 1157 1256: gap of 100 bp
* 1257 1891: contig of 635 bp in length
* 1892 1991: gap of 100 bp
* 1992 2942: contig of 951 bp in length
* 2943 3042: gap of 100 bp
* 3043 4004: contig of 962 bp in length
* 4005 4104: gap of 100 bp
* 4105 4797: contig of 693 bp in length
* 4798 4897: gap of 100 bp
* 4898 5626: contig of 729 bp in length
* 5627 5726: gap of 100 bp
* 5727 6421: contig of 695 bp in length
* 6422 6521: gap of 100 bp
* 6522 7622: contig of 1101 bp in length
* 7623 7722: gap of 100 bp
* 7723 8353: contig of 631 bp in length
* 8354 8453: gap of 100 bp
* 8454 9092: contig of 639 bp in length
* 9093 9192: gap of 100 bp
* 9193 10104: contig of 912 bp in length
* 10105 10204: gap of 100 bp
* 10205 10848: contig of 644 bp in length
* 10849 10948: gap of 100 bp
* 10949 11899: contig of 951 bp in length
* 11900 11999: gap of 100 bp
* 12000 12601: contig of 602 bp in length
* 12602 12701: gap of 100 bp
* 12702 13401: contig of 700 bp in length
* 13402 13501: gap of 100 bp
* 13502 13936: contig of 435 bp in length
* 13937 14036: gap of 100 bp
* 14037 14681: contig of 645 bp in length
* 14682 14781: gap of 100 bp
* 14782 15812: contig of 1031 bp in length
* 15813 15912: gap of 100 bp
* 15913 16579: contig of 667 bp in length
* 16580 16679: gap of 100 bp
* 16680 17502: contig of 823 bp in length
* 17503 17602: gap of 100 bp
* 17603 18647: contig of 1045 bp in length
* 18648 18747: gap of 100 bp
* 18748 19879: contig of 1132 bp in length
* 19880 19979: gap of 100 bp
* 19980 21001: contig of 1022 bp in length
* 21002 21101: gap of 100 bp

```



-----  
\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 57 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1478: contig of 1478 bp in length  
\* 1479 1578: gap of unknown length  
\* 1579 2917: contig of 1339 bp in length  
\* 2918 3017: gap of unknown length  
\* 3018 4096: contig of 1079 bp in length  
\* 4097 4196: gap of unknown length  
\* 4197 5642: contig of 1446 bp in length  
\* 5643 5742: gap of unknown length  
\* 5743 6339: contig of 1197 bp in length  
\* 6340 7039: gap of unknown length  
\* 7040 8481: contig of 1442 bp in length  
\* 8482 10096: contig of 1515 bp in length  
\* 10097 10196: gap of unknown length  
\* 10197 11452: contig of 1256 bp in length  
\* 11453 11552: gap of unknown length  
\* 11553 12648: contig of 1096 bp in length  
\* 12649 12748: gap of unknown length  
\* 12749 14133: contig of 1385 bp in length  
\* 14134 14233: gap of unknown length  
\* 14234 15551: contig of 1318 bp in length  
\* 15552 15651: gap of unknown length  
\* 15652 17024: contig of 1373 bp in length  
\* 17025 17124: gap of unknown length  
\* 17125 18147: contig of 1023 bp in length  
\* 18148 18247: gap of unknown length  
\* 18248 19923: contig of 1676 bp in length  
\* 19924 20023: gap of unknown length  
\* 20024 21045: contig of 1022 bp in length  
\* 21046 21145: gap of unknown length  
\* 21146 22252: contig of 1147 bp in length  
\* 22253 22392: gap of unknown length  
\* 22393 23545: contig of 1153 bp in length  
\* 23546 23645: gap of unknown length  
\* 23646 25288: contig of 1643 bp in length  
\* 25289 25388: gap of unknown length  
\* 25389 26988: contig of 1600 bp in length  
\* 26989 27088: gap of unknown length  
\* 27089 29136: contig of 2048 bp in length  
\* 29137 29236: gap of unknown length  
\* 29237 30361: contig of 1125 bp in length  
\* 30362 30461: gap of unknown length  
\* 30462 31728: contig of 1267 bp in length  
\* 31729 31828: gap of unknown length  
\* 31829 33326: contig of 1498 bp in length  
\* 33327 33426: gap of unknown length  
\* 33427 34972: contig of 1546 bp in length  
\* 34973 35072: gap of unknown length  
\* 35073 37098: contig of 2026 bp in length  
\* 37099 37198: gap of unknown length  
\* 37199 38976: contig of 1678 bp in length  
\* 38977 38976: gap of unknown length  
\* 40520 40620: contig of 1544 bp in length  
\* 40521 40620: gap of unknown length  
\* 40621 41712: contig of 1092 bp in length  
\* 41713 41812: gap of unknown length  
\* 41813 43711: contig of 1899 bp in length  
\* 43712 43811: gap of unknown length  
\* 43812 45722: contig of 1911 bp in length  
\* 45723 45822: gap of unknown length  
\* 45823 47646: contig of 1824 bp in length  
\* 47647 47646: gap of unknown length

47747 49427: contig of 1681 bp in length  
\* 49428 49527: gap of unknown length  
\* 49528 51247: contig of 1720 bp in length  
\* 51248 51347: gap of unknown length  
\* 51348 53372: contig of 2025 bp in length  
\* 53373 53472: gap of unknown length  
\* 53473 55965: contig of 2493 bp in length  
\* 55966 56065: gap of unknown length  
\* 56066 58704: contig of 2539 bp in length  
\* 58705 61433: contig of 2729 bp in length  
\* 61434 61533: gap of unknown length  
\* 61534 63097: contig of 1564 bp in length  
\* 63098 63197: gap of unknown length  
\* 63198 65272: contig of 2075 bp in length  
\* 65273 67765: contig of 2393 bp in length  
\* 67766 67865: gap of unknown length  
\* 67866 68952: contig of 1087 bp in length  
\* 68953 69052: gap of unknown length  
\* 69054 72102: contig of 3050 bp in length  
\* 72103 72202: gap of unknown length  
\* 72203 74585: contig of 2383 bp in length  
\* 74586 74686: gap of unknown length  
\* 74687 77512: contig of 2727 bp in length  
\* 77513 80330: contig of 2818 bp in length  
\* 80331 80430: gap of unknown length  
\* 80431 82126: contig of 1696 bp in length  
\* 82127 82226: gap of unknown length  
\* 82227 84702: contig of 2476 bp in length  
\* 84703 84802: gap of unknown length  
\* 84803 88989: contig of 4187 bp in length  
\* 88990 92993: contig of 3904 bp in length  
\* 92994 93093: gap of unknown length  
\* 93094 96037: contig of 2944 bp in length  
\* 96038 96137: gap of unknown length  
\* 96138 100350: contig of 4213 bp in length  
\* 100351 100450: gap of unknown length  
\* 100451 104033: contig of 3583 bp in length  
\* 104034 104133: gap of unknown length  
\* 104134 106965: contig of 2832 bp in length  
\* 106966 107065: gap of unknown length  
\* 107066 112233: contig of 5168 bp in length

Query Match 6.1%; Score 85.4; DB 2; Length 127354;  
Best Local Similarity 45.4%; Pred. No. 6.7e-06;  
Matches 308; Conservative 0; Mismatches 371; Indels 0; Gaps 0;

Qy 614 ATCCAGTAAAGTTAATGCACACCTTGCCGCAATTAACCTGCTAATGTTGCTTAAG 673  
Db 118142 AGCAAGACTAAACTGAATGGTTACTACTGCTACTACTACTGCTGCTACTACTACTAG 118201

Qy 674 CTACTTTAGGTAAATGATGCTACATAACCCGCAATTAATGACGTTGATGCTGATGTTA 733  
Db 118202 CTGCTATTACTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTAG 118261

Qy 734 CTATAAGTCTGCTGGAGTAAATAATTTGGGTAGCACAACACACTGAATGTACTAATTGTG 793  
Db 118262 CTACTGCTGCTACTACTACTGCTGCTACTACTACTACTACTACTGCTGCTACTACTAG 118321

Qy 794 CTCCTAATCTTTACAATAAATGCTCTCTAATTTCAATCCAGGTAATAGTACATGCTTAC 853  
Db 118322 CTGCTGCTACTACTACTACTGCTGCTACTACTACTACTACTACTACTACTACTACTAG 118381

Qy 854 CTGCCCCAGCAATAAAGATTATGGTCTGAAGCCACTGCAGGTGGTGGCGGCTACTTTAG 913  
Db 118382 CTACTGCTGCTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTAG 118441

Qy 914 CCAATAATGTAATTTGTCATGCCCTGATGGTACTGCAATTTGCTAGTGGAGCAACTAATT 973  
Db 118442 CTGCTACTACTACTGTTGCTACTACTACTACTACTACTACTACTACTACTACTACTAG 118501







